

Sequence Listing

- <110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Occupation	Unemployed	10	0	20
Income	Low	10	0	20
Health status	Good	15	0	30
Stress level	High	10	0	20
Life satisfaction	Low	10	0	20
Depression	High	10	0	20
Loneliness	High	10	0	20
Self-esteem	Low	10	0	20
Resilience	Low	10	0	20
Optimism	Low	10	0	20
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Management	Low	10	0	20
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Decision-making	Low	10	0	20
Problem-solving	Low	10	0	20
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 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
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35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
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Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
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Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
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Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
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Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
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Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315
Pro	Lys	Ala	Val											

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggaattca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaattc acccgtctta ccagctctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
 agtgcacatg aactatcgcc agaagggcgt gattgacgtc ttctgcatg 800
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met	Ala	Ala	Cys	Glu	Gly	Arg	Arg	Ser	Gly	Ala	Leu	Gly	Ser	Ser
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Gln	Ser	Asp	Phe	Leu	Thr	Pro	Pro	Val	Gly	Gly	Ala	Pro	Trp	Ala
			20						25					30

Val	Ala	Thr	Thr	Val	Val	Met	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				35				40						45

His	Arg	Asp	Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr
			50					55						60

Asp	Asn	Ser	Lys	Ser	Trp	Arg	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp
			65						70					75

Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu
			80					85						90

Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala
			95					100						105

	395		400		405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu Ala			
	410	415			420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys Lys			
	425	430			435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu Phe			
	440	445			450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser Tyr			
	455	460			465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln Glu			
	470	475			480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val Arg			
	485	490			495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe Val			
	500	505			510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His Leu			
	515	520			525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His Gly			
	530	535			540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu Thr			
	545	550			555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro Glu			
	560	565			570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp Val			
	575	580			585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro Glu Thr			
	590	595			600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg Lys			
	605	610			615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg Phe			
	620	625			630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val Gln			
	635	640			645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe Phe			
	650	655			660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp Asp			
	665	670			675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu Ala			
	680	685			690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccggggccg gccgggctgc gagcgctgc 50
cccatgcgcc gccgcctctc cgcaogatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
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 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

	140		145		150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp	155		160		165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala	170		175		180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His	185		190		195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His	200		205		210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly	215		220		225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu	230		235		240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe	245		250		255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg	260		265		270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly	275		280		285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu	290		295		300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp	305		310		315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser	320		325		

<210> 18

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 18

gcgaacgctt cgaggagtcc tgg 23

<210> 19

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

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Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
	590	595	600		
Ala Leu Lys Val	Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr		
	605	610	615		

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

ctatgcggcc ctcttctgcc tctcggcctc catcatctac cccaccacct 500
 atgtccagtt cctgtcccac ggccgttcgc gggaccaogc catcgccgcc 550
 accttcttct cctgcatcgc gtgtgtggct tacgccaccg aagtggcctg 600
 gaccggggcc cggcccggcg agatcactgg ctatatggcc accgtaccgc 650
 ggctgctgaa ggtgctggag accttcgttg cctgcatcat cttcgcgttc 700
 atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtgcgt 750
 ggcggtgtac gccatctgct tcatcctagc ggccatogcc atcctgctga 800
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 tcggggctgg ccttgctgtc tgtcctcctc tatgccaccg cccttggtct 900
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 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
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 Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg
 20 25 30
 Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

cgcagcctgg gccactgga ggcccaggac tcaactetaca actcgcccct 2200
 cacagagtcc tgcctttccc ccgcggagga ggagccagcc ccctgcaagg 2250
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Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245						250					255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
			335											

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct

<400> 34
 tgtcctttgt cccagacttc tgtcc 25

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 35
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
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ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cactttaac 100
ccatctgttt tototaatgc acgacagatt cctttcagac aggacaactg 150
tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200
tactagccat tgtgagcttc agttttcttca tctgcaaaat gggcataata 250
caatctattc ttgccacatc aagggtattgt tattccttta aaaaaaac 300

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330
Arg	Thr	Ser	Val											

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gtcctcttgg gagatgtatg cttactctct 250
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 tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
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 tattcatgac tttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

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ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
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			65						70					75
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
			80						85					90
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
			95						100					105
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
			110						115					120
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
			125						130					135
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
				140					145					150
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
				155					160					165
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser
				170					175					180
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln
				185					190					195
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly
				200					205					210
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln
				215					220					225
Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
				230					235					240
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser
				245					250					255
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly
				260					265					270
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser
				275					280					285
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser
				290					295					300
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly
				305					310					315
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His
				320					325					330
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly
				335					340					345

Glu Ser Gly Ile	Gln Gly Phe Arg Gly	Gln Gly Val Ser Ser	Asn
350	355	360	
Met Arg Glu Ile	Ser Lys Glu Gly Asn	Arg Leu Leu Gly Gly	Ser
365	370	375	
Gly Asp Asn Tyr	Arg Gly Gln Gly Ser	Ser Trp Gly Ser Gly	Gly
380	385	390	
Gly Asp Ala Val	Gly Gly Val Asn Thr	Val Asn Ser Glu Thr	Ser
395	400	405	
Pro Gly Met Phe	Asn Phe Asp Thr Phe	Trp Lys Asn Phe Lys	Ser
410	415	420	
Lys Leu Gly Phe	Ile Asn Trp Asp Ala	Ile Asn Lys Asp Gln	Arg
425	430	435	
Ser Ser Arg Ile	Pro		
440			

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
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 ctctcctgct ggcctgcac cggagcttgg tgttgctgca ggagagtgg 200
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 gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
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gagttctgtc aaaggaagag ccctggggct gtgcggggcg tgcttccaga 850
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<400> 54

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Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu
				20					25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
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<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
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cgacacctac ccctcagcag acgccggaga gaaatgagta gcaacaaaga 200
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<400> 57

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gcagaggggc gaggctgaag ccgagtggcc cgaggtgtct gaggggctgg 150
ggcaaagggtg aaagagtttc agaacaagct tcctggaacc catgacccat 200
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<212> PRT

<213> Homo sapiens

<400> 58

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Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala	
				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val	Thr	Gly	Tyr	Asn	Lys	Thr	Arg	Phe	Leu	Leu	Ser	Asn	Leu	Leu	275	280	285
Ile	Asp	Thr	Thr	Ser	Glu	Glu	Asp	Ser	Gly	Thr	Tyr	Arg	Cys	Met	290	295	300
Ala	Asp	Asn	Gly	Val	Gly	Gln	Pro	Gly	Ala	Ala	Val	Ile	Leu	Tyr	305	310	315
Asn	Val	Gln	Val	Phe	Glu	Pro	Pro	Glu	Val	Thr	Met	Glu	Leu	Ser	320	325	330
Gln	Leu	Val	Ile	Pro	Trp	Gly	Gln	Ser	Ala	Lys	Leu	Thr	Cys	Glu	335	340	345
Val	Arg	Gly	Asn	Pro	Pro	Pro	Ser	Val	Leu	Trp	Leu	Arg	Asn	Ala	350	355	360
Val	Pro	Leu	Ile	Ser	Ser	Gln	Arg	Leu	Arg	Leu	Ser	Arg	Arg	Ala	365	370	375
Leu	Arg	Val	Leu	Ser	Met	Gly	Pro	Glu	Asp	Glu	Gly	Val	Tyr	Gln	380	385	390
Cys	Met	Ala	Glu	Asn	Glu	Val	Gly	Ser	Ala	His	Ala	Val	Val	Gln	395	400	405
Leu	Arg	Thr	Ser	Arg	Pro	Ser	Ile	Thr	Pro	Arg	Leu	Trp	Gln	Asp	410	415	420
Ala	Glu	Leu	Ala	Thr	Gly	Thr	Pro	Pro	Val	Ser	Pro	Ser	Lys	Leu	425	430	435
Gly	Asn	Pro	Glu	Gln	Met	Leu	Arg	Gly	Gln	Pro	Ala	Leu	Pro	Arg	440	445	450
Pro	Pro	Thr	Ser	Val	Gly	Pro	Ala	Ser	Pro	Lys	Cys	Pro	Gly	Glu	455	460	465
Lys	Gly	Gln	Gly	Ala	Pro	Ala	Glu	Ala	Pro	Ile	Ile	Leu	Ser	Ser	470	475	480
Pro	Arg	Thr	Ser	Lys	Thr	Asp	Ser	Tyr	Glu	Leu	Val	Trp	Arg	Pro	485	490	495
Arg	His	Glu	Gly	Ser	Gly	Arg	Ala	Pro	Ile	Leu	Tyr	Tyr	Val	Val	500	505	510
Lys	His	Arg	Lys	Gln	Val	Thr	Asn	Ser	Ser	Asp	Asp	Trp	Thr	Ile	515	520	525
Ser	Gly	Ile	Pro	Ala	Asn	Gln	His	Arg	Leu	Thr	Leu	Thr	Arg	Leu	530	535	540
Asp	Pro	Gly	Ser	Leu	Tyr	Glu	Val	Glu	Met	Ala	Ala	Tyr	Asn	Cys	545	550	555
Ala	Gly	Glu	Gly	Gln	Thr	Ala	Met	Val	Thr	Phe	Arg	Thr	Gly	Arg			

560										565					570				
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln					
				575					580					585					
Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Ser	Gln	Pro	Asp				
				590					595					600					
His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile					
				605					610					615					
Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg					
				620					625					630					
Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys					
				635					640					645					
Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile					
				650					655					660					
Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly					
				665					670					675					
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu					
				680					685					690					
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr					
				695					700					705					
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr					
				710					715					720					
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met					
				725					730					735					
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr					
				740					745					750					
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys					
				755					760					765					
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His					
				770					775					780					
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn					
				785					790					795					
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr					
				800					805					810					
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro					
				815					820					825					
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg					
				830					835					840					
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro					
				845					850					855					

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gccagttct	ggtcagcctc	cgtctcatgc	cagtcccagg	accagactgc	550
cgtgcgcctc	gccctggagc	agattgacct	cattcaccgc	atgtgtgcct	600
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tgctgacaca	gtcgggtccc	gcagagggtc	ctgtggcaaa	gcctcacaaa	1600
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<210> 63

<211> 487

<212> PRT

<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
125 130 135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
140 145 150

Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
155 160 165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
170 175 180

Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
185 190 195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
200 205 210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
215 220 225

Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
230 235 240

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
245 250 255

Cys Gln Lys Ile

<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens

<400> 71
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acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
cttccttcta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250
atatttttagt aattcatatg ttttagatta taggttttaa cataacttgtg 300
aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
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gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
ctcaagcccc caacatccca gtccctcagtc ctcagtcctc ttgacttcaa 600
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
agcaccagag ccaggcagtc actgttcctc ctccctgggtt ggagtccttt 700
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
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tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
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ccgtcattac ctccctcagc ctgacaagct catcactgaa ttctgctagt 1150
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gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
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ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
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Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
 <211> 50

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Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
				95					100					105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
				110					115					120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
				125					130					135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu
				140					145					150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp
				155					160					165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu
				170					175					180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala
				185					190					195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser
				200					205					210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val
				215					220					225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln
				230					235					240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu
				245					250					255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu
				260					265					270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn
				275					280					285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg
				290					295					300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu
				305					310					315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp
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Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys				
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<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200
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<212> DNA

<213> Homo sapiens

<400> 83

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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggcgcctg gggcgtcaat cggaccctga 250
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<212> PRT

<213> Homo sapiens

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<211> 22

<212> DNA

<213> Artificial

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<400> 90

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<210> 91

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<222> 1-26

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<213> Artificial

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<222> 1-47

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<400> 93

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<210> 94

<211> 3037

<212> DNA

<213> Homo sapiens

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Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
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Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	
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<212> DNA

<213> Homo sapiens

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
				95					100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
				110					115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
				125					130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
				140					145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
				155					160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
				170					175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
				185					190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
				200					205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
				215					220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
				230					235					240

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu
				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
				170					175					180
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
				185					190					195
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

				200					205					210
Ile	Leu	Glu	His	Leu 215	Tyr	Pro	Thr	Met	Asp 220	Ser	Gly	Glu	Trp	Asp 225
Val	Leu	Ile	Ala	His 230	Phe	Leu	Gly	Val	Asp 235	His	Cys	Gly	His	Lys 240
His	Gly	Pro	His	His 245	Pro	Glu	Met	Ala	Lys 250	Lys	Leu	Ser	Gln	Met 255
Asp	Gln	Val	Ile	Gln 260	Gly	Leu	Val	Glu	Arg 265	Leu	Glu	Asn	Asp	Thr 270
Leu	Leu	Val	Val	Ala 275	Gly	Asp	His	Gly	Met 280	Thr	Thr	Asn	Gly	Asp 285
His	Gly	Gly	Asp	Ser 290	Glu	Leu	Glu	Val	Ser 295	Ala	Ala	Leu	Phe	Leu 300
Tyr	Ser	Pro	Thr	Ala 305	Val	Phe	Pro	Ser	Thr 310	Pro	Pro	Glu	Glu	Pro 315
Glu	Val	Ile	Pro	Gln 320	Val	Ser	Leu	Val	Pro 325	Thr	Leu	Ala	Leu	Leu 330
Leu	Gly	Leu	Pro	Ile 335	Pro	Phe	Gly	Asn	Ile 340	Gly	Glu	Val	Met	Ala 345
Glu	Leu	Phe	Ser	Gly 350	Gly	Glu	Asp	Ser	Gln 355	Pro	His	Ser	Ser	Ala 360
Leu	Ala	Gln	Ala	Ser 365	Ala	Leu	His	Leu	Asn 370	Ala	Gln	Gln	Val	Ser 375
Arg	Phe	Leu	His	Thr 380	Tyr	Ser	Ala	Ala	Thr 385	Gln	Asp	Leu	Gln	Ala 390
Lys	Glu	Leu	His	Gln 395	Leu	Gln	Asn	Leu	Phe 400	Ser	Lys	Ala	Ser	Ala 405
Asp	Tyr	Gln	Trp	Leu 410	Leu	Gln	Ser	Pro	Lys 415	Gly	Ala	Glu	Ala	Thr 420
Leu	Pro	Thr	Val	Ile 425	Ala	Glu	Leu	Gln	Gln 430	Phe	Leu	Arg	Gly	Ala 435
Arg	Ala	Met	Cys	Ile 440	Glu	Ser	Trp	Ala	Arg 445	Phe	Ser	Leu	Val	Arg 450
Met	Ala	Gly	Gly	Thr 455	Ala	Leu	Leu	Ala	Ala 460	Ser	Cys	Phe	Ile	Cys 465
Leu	Leu	Ala	Ser	Gln 470	Trp	Ala	Ile	Ser	Pro 475	Gly	Phe	Pro	Phe	Cys 480
Pro	Leu	Leu	Leu	Thr 485	Pro	Val	Ala	Trp	Gly 490	Leu	Val	Gly	Ala	Ile 495

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgct aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcac cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactocaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatcaaac agaacgtggg cccagtgtgt gaccaaccac acgctgggtc 400
tcacctggct ggagcogaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatoca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcggaacct gaggccccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtccct 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggagcggtt 1100
ggcagctttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
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 cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atgggtgggc 1650
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<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165

<211> 21
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct

 <400> 105
 cgctgctgct gttgctcctg g 21

 <210> 106
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 106
 cagtgtgccca ggactttg 18

 <210> 107
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 107
 agtcgcaggc agcgttgg 18

 <210> 108
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 108
 ctctctccgag tctgtgtgct cctgc 25

 <210> 109
 <211> 51
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacad 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
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cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150
gtcctgggg ggcccagatc atcgggggcc acgaggtagc cccccactcc 200
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gggagaaggg ccaggcccc caccgcgggg acacggtgcc ggtggtctgg 550
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aaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
cgtgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

gagagcaggt gcaggtgtca tcccaggttc aggctctgca cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala	
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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	
				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155					160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	
His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
 gaagttcgcg agcgctggca tgtggtcctg gggcgcggtt ggcggcgctg 50
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgccccg 150
 agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200
 cggtgcggg acctgactag attctacgac aaggtacttt ctttgcata 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcatTT actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccaggg tgtctttcag 500
 agagtcactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagttct 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

tacattatat aaggattttt ttttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

530

535

540

Ser Pro Glu Asp

<210> 119
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 119
 cgggacagga gaccagaaa ggg 23

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 121
 ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 122
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 tcccaccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
 gaatcgccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
 ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
gctcaagttt tcacttatca tctattccac cgtgttcttg ctgattgggg 300
ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550
gaccattgac ttcctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagtgc 650
aagtgtctgt gcggggagga ctaccgagat tggagcaaga atcagtacca 700
cgactgcagt gccctggac ccctggcctg tggggtgccc tacacctgct 750
gcatcaggaa cagcagagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
atcgacaagg agcgtttcag tgtgcaggat gtcactacg tgcggggctg 850
caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
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ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggtgct 1600
tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcac 1700
 gtcttattct tgcccttccc ccaaccagtt tgtaatacaa acaataaaaa 1750
 catgttttgt ttgttttta aaaaaaaaa 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
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 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr			
	245	250		255	
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp			
	260	265		270	
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly			
	275	280		285	
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn				
	290				

<210> 124

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 124

atcatctatt ccaccgtgtt ctggc 25

<210> 125

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 125

gacagagtgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 126

cctgtctgtg ggcatttatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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gctgccctct gacacctggg aagatggccg gcccggtggac ottcaccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtctgaagc acatcatctg gctgaaggtc atcacagcta 350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
gaccatcgtg gaggttccaca tgacgactga ggccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgcc tggctcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttct 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
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ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
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gaaacccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu	170	175	180	
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	185	190	195	
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	200	205	210	
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	215	220	225	

[illegible][illegible]

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cttggcgctg	gcggtactgg	cccccgagc	aggggagcag	aggcggagag	200
cagccaaagc	gcccaatgtg	gtgctggctg	tgagcgactc	cttcgatgga	250
aggttaacat	ttcatccagg	aagtcaggta	gtgaaacttc	cttttatcaa	300
ctttatgaag	acacgtggga	cttcctttct	gaatgcctac	acaaactctc	350
caatttggtg	cccatcacgc	gcagcaatgt	ggagtggcct	cttcactcac	400
ttaacagaat	cttgaataa	ttttaaggg	ctagatccaa	attatacaac	450
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aactggacta	tacttcagga	catcactcca	ttagtaatcg	tgtggaagcg	550
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gcatgtacga	ggctagtgc	catgttccgc	ttttgatgat	gggaccagga	1150
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ccctaccatg	cttgatattg	ctggaattcc	tctgcctcag	aacctgagtg	1250
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gatccagatg	aattaacaaa	tgttgctgta	aaatttccag	aaattactta	1500
ttctttggat	cagaagcttc	attccattat	aaactaccct	aaagtttctg	1550

atcccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggata 550
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 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450
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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1				5					10					15

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60				
Ile	Thr	Gln	Cys	Asp 65	Ile	Tyr	Ser	Thr	Leu 70	Leu	Gly	Leu	Pro	Ala 75
Asp	Ile	Gln	Ala	Ala 80	Gln	Ala	Met	Met	Val 85	Thr	Ser	Ser	Ala	Ile 90
Ser	Ser	Leu	Ala	Cys 95	Ile	Ile	Ser	Val	Val 100	Gly	Met	Arg	Cys	Thr 105
Val	Phe	Cys	Gln	Glu 110	Ser	Arg	Ala	Lys	Asp 115	Arg	Val	Ala	Val	Ala 120
Gly	Gly	Val	Phe	Phe 125	Ile	Leu	Gly	Gly	Leu 130	Leu	Gly	Phe	Ile	Pro 135
Val	Ala	Trp	Asn	Leu 140	His	Gly	Ile	Leu	Arg 145	Asp	Phe	Tyr	Ser	Pro 150
Leu	Val	Pro	Asp	Ser 155	Met	Lys	Phe	Glu	Ile 160	Gly	Glu	Ala	Leu	Tyr 165
Leu	Gly	Ile	Ile	Ser 170	Ser	Leu	Phe	Ser	Leu 175	Ile	Ala	Gly	Ile	Ile 180
Leu	Cys	Phe	Ser	Cys 185	Ser	Ser	Gln	Arg	Asn 190	Arg	Ser	Asn	Tyr	Tyr 195
Asp	Ala	Tyr	Gln	Ala 200	Gln	Pro	Leu	Ala	Thr 205	Arg	Ser	Ser	Pro	Arg 210
Pro	Gly	Gln	Pro	Pro 215	Lys	Val	Lys	Ser	Glu 220	Phe	Asn	Ser	Tyr	Ser 225
Leu	Thr	Gly	Tyr	Val 230										

<210> 135

 $\langle 211 \rangle$ 610

<212> DNA

<213> Homo sapiens

<400> 135

gcactgctgc tgtcccatca gctgctctga agctccatgg tgcccagaat 50

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aaatcatcgc tcccgctggc tcagaacccat ggctgtgcca gccggcacc 150

aggtgtggag acaagatcta caacccttg gagcagtget gttacaatga 200

cgccatcgtg tccctgagcg agacccgcca atgtgggtccc ccctgcacct 250

tetggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaac 300

gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

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 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtctgtccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctacgcccgg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ctttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
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 ctttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20					25						30
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105
Cys	Arg	Ser	Val	Ser										
			110											

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 gttgccccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850
 ggaaggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
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<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
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 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met Glu	
155		160	165
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val Val	
170		175	180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala Ala	
185		190	195
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro Leu	
200		205	210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn Arg	
215		220	225
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly Ile	
230		235	240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile Pro	
245		250	255
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg Gln	
260		265	270
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr Pro	
275		280	285
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu Asp	
290		295	300
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile	
305		310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ccttctgccc ctcccttctt gccaccgct gcttcttggc 150
 ccttctccga ccccgctcta gcagcagacc tcctgggggc tgtgggttga 200
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cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
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agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700
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aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatocatgtt ccagtgatgc 900
tgggagaaaag agaggcccg gcaccccagc cccactggc ctcagcgccc 950
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gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
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taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
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aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
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cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

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 ttttaagggtcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met	Asp	Ser	Leu	Arg	Lys	Met	Leu	Ile	Ser	Val	Ala	Met	Leu	Gly
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Ala	Gly	Ala	Gly	Val	Gly	Tyr	Ala	Leu	Leu	Val	Ile	Val	Thr	Pro
				20					25					30
Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln
				35					40					45
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu
				50					55					60
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala
				65					70					75
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly
				80					85					90
Arg	Ser	Pro												

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

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 caggctgcca tggggcccag caccctctc ctcactctgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
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 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctgggtcta tggaccaagg atccactggg 600
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 ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700
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 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
 aaccgaacag tggtgagacg ctcagtattc ccagcagagg ggctgatccc 900
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 aaggtctttg ggctgtctat gccaccggg aggatgacag gcacttgtgt 1000
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 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

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acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
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cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
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cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
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 agaggggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgcc tggagaagga catgaagaac gtcgtggggg 200
 tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
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 ctccggatgg gtgtttgaga atccctcaat aggcctgctg gagctctggg 350
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 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
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<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
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 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccatcccc tcgcatggct ggatttacc 200
tggcccagta gttcatggct actggttcog ggaaggggcc aatacagacc 250
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actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttcttct 400
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gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
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cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
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Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
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 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
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 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250
 gagggaggat cgggtcatcc agaagaaaat cctgatgcgg aagacggagg 300
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 tgggggcctg ctccacatgg gaaagottgt gggtaggaat tctgatacca 450
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 tcggaggagg acattttcac gccctgcag acgggaagct gcgttccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
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 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct.

<400> 165
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<210> 166
 <211> 25
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 166
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<210> 167
 <211> 50
 <212> DNA
 <213> Artificial

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 <222> 1-50
 <223> Synthetic construct.

<400> 167
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<210> 168
 <211> 45
 <212> DNA
 <213> Artificial

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 <222> 1-45
 <223> Synthetic construct.

<400> 168
 ctgtccttca ccctggagga ggaggatata acaggacct ggtac 45

<210> 169
 <211> 1204
 <212> DNA
 <213> Homo sapiens

<400> 169

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aaatatattgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
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His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

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<211> 24
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<223> Synthetic construct.

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<400> 174
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<210> 175
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<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

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<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcagat gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

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gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
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<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

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<222> 1-18

<223> Synthetic construct.

<400> 183

cctttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<220>
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 <222> 1-18
 <223> Synthetic construct.

<400> 184
 gatgtctgcc accccaag 18

<210> 185
 <211> 27
 <212> DNA
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 <222> 1-27
 <223> Synthetic construct.

<400> 185
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<210> 186
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 186
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<210> 187
 <211> 52
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-52
 <223> Synthetic construct.

<400> 187
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 cc 52

<210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 188
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 ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
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 ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

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1				5					10					15
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65					70					

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
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<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
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gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
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gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
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 tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

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Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

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 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

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Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Cys Ile Pro Leu Asp	Lys Gly Phe Ser Cys Glu Cys Val Pro Gly	
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatagc cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct ttctcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttctctaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtcccg ttcctcccaa tattccttct caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaat 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
1				5					10					15	
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200
tttgcatagag ttctctggtta atttgcata gagatatggg cctgtggtct 250
ccttctggtt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg cctcctcct aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa agaacgaaa aggaaggaac ttcagtcaac atattttcat 800
tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

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ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tggtcgaact 1050
gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
tggtacttca ggatccta atcttgccat ctccacacaa gtttgatcca 1200
gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggtt 1250
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cagtacttct tagtgattg gtgaagagac tgcacctact ttctgtggag 1350
ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
agcttggtatc actgtctcaa agagatatta aaattttata catttaaaat 1450
cattgttaaa ttgattgagg aaaacaacca ttttaaaaaa atctatgttg 1500
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<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

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Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
 1             5             10             15
Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
          20             25             30
Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
          35             40             45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
          50             55             60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
          65             70             75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
          80             85             90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
          95             100            105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
          110            115            120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
          125            130            135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

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Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
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 tcagggcttg tgccctctcg cttcctgacg ctctggcgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgctct ctgtcacct gggcctcttt gcagtggagc tggccggttt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttccccctcg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgtttttag tagtaattaag acttatatac agtttttaggg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	
				50					55					60	
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	
				65					70					75	
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	
				80					85					90	
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	
				95					100					105	
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	
				110					115					120	
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	
				125					130					135	
Lys	Lys	Lys	Pro	Phe											
				140											

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
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 gaccggcct gctgcagccc catagtgtccc cggaacgagt ggaaggccct 150
 ggcatcagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
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 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
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 acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
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 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
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Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195
Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cgccccggg tgccctcgaa 200

gcggggccac atctcaccta agtcccgcc catggccaat tccactctcc 250
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gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
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tggtctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800
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<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

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Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
 gcgccgccgc cgccgtcgct cctgcagcgc tgtcgacctc gccgctagca 250
 tcttcccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
 agcgccagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350
 ccgggcgctg tccgcggtgc cggccgtgct gctggctctc acgctgccgg 400
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
 aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500
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tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
gaatthttatt tgthttagtht taaaagactg gcaaccaggt ctaaggatta 1300
gaaaactcta aagthtctgac thcaatcaac ggthtagtgtg atactgccaa 1350
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ggaattagtht tgthttggtc thgtaaaaaa cthggatttht thththtcagt 1450
aactggthatt atgtththctc thaaaataag gtaatgaatg gcttgccac 1500
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gaatgcttca tagthgtatt thaatgtat atgtgaaaga gtcaththt 1600
ccaagthata ththtctaaga agaagaatag atcataaatc tgacaaggaa 1650
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cgtagacatg accacttht thactggthg tgggatgctg thgtthtctaa 1850
thtatactat ththtcaaggc thctgtthgta thtgaagtat catctggtht 1900
thgccttaact cthtaaatg thtatathth thctgtthtagc thaatathaa 1950
thcaaatac ccatatctaa athtagtgca atathctgtc ththgtatag 2000
gtcatatgaa thcataaaat thththtgthc thgttatagaa thaaagathaa 2050
tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
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Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
				20				25						30
Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35				40						45
Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55						60

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cgggtggccat gactgcggcc gtgtttcttcg gctgcgcctt cattgccttc 50
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
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tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
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tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700
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actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
1 5 10 15

Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30

Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120

Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135

Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150

Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165

Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180

Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195

His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210

Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225

Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
gtctgtgaac gtcctgaaca agcagaaggg ggcgcggttg ctgtttgtgg 300
tccgccagaa ggaggctgtg gtgtccttcc aggtgccct aatcctgcga 350
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tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
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agcagcacag cccagtact tcaagtatga gttccctgaa ggcgtggact 600
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tccattcagg atgtgctgtg tcctgtctat gacctggaca acaacgtagc 700
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20				25						30

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30

Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp
305 310 315

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn
				320					325					330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile
				335					340					345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala
				350					355					360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr
				365					370					375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala
				380					385					390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu
				395					400					405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met
				410					415					420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val
				425					430					435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile
				440					445					450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro
				455					460					465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu
				470					475					480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr
				485					490					495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val
				500					505					510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser
				515					520					525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly
				530					535					540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val
				545					550					555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu
				560					565					570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr
				575					580					585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu
				590					595					600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttctgag 250
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tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

200					205					210				
Lys	Trp	Glu	Lys	Pro	Phe	His	Leu	Glu	Tyr	Thr	Arg	Lys	Asn	Phe
				215					220					225
Pro	Phe	Leu	Val	Gly	Glu	Gln	Val	Thr	Val	Gln	Val	Pro	Met	Met
				230					235					240
His	Gln	Lys	Glu	Gln	Phe	Ala	Phe	Gly	Val	Asp	Thr	Glu	Leu	Asn
				245					250					255
Cys	Phe	Val	Leu	Gln	Met	Asp	Tyr	Lys	Gly	Asp	Ala	Val	Ala	Phe
				260					265					270
Phe	Val	Leu	Pro	Ser	Lys	Gly	Lys	Met	Arg	Gln	Leu	Glu	Gln	Ala
				275					280					285
Leu	Ser	Ala	Arg	Thr	Leu	Ile	Lys	Trp	Ser	His	Ser	Leu	Gln	Lys
				290					295					300
Arg	Trp	Ile	Glu	Val	Phe	Ile	Pro	Arg	Phe	Ser	Ile	Ser	Ala	Ser
				305					310					315
Tyr	Asn	Leu	Glu	Thr	Ile	Leu	Pro	Lys	Met	Gly	Ile	Gln	Asn	Ala
				320					325					330
Phe	Asp	Lys	Asn	Ala	Asp	Phe	Ser	Gly	Ile	Ala	Lys	Arg	Asp	Ser
				335					340					345
Leu	Gln	Val	Ser	Lys	Ala	Thr	His	Lys	Ala	Val	Leu	Asp	Val	Ser
				350					355					360
Glu	Glu	Gly	Thr	Glu	Ala	Thr	Ala	Ala	Thr	Thr	Thr	Lys	Phe	Ile
				365					370					375
Val	Arg	Ser	Lys	Asp	Gly	Pro	Ser	Tyr	Phe	Thr	Val	Ser	Phe	Asn
				380					385					390
Arg	Thr	Phe	Leu	Met	Met	Ile	Thr	Asn	Lys	Ala	Thr	Asp	Gly	Ile
				395					400					405
Leu	Phe	Leu	Gly	Lys	Val	Glu	Asn	Pro	Thr	Lys	Ser			
				410					415					

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

				365					370					375
Thr	Asn	Ser	Glu	Ser 380	Ser	Thr	Val	Ser	Ser 385	Gly	Ala	Ser	Thr	Ala 390
Thr	Asn	Ser	Glu	Ser 395	Ser	Thr	Thr	Ser	Ser 400	Gly	Val	Ser	Thr	Ala 405
Thr	Asn	Ser	Glu	Ser 410	Ser	Thr	Thr	Ser	Ser 415	Gly	Ala	Ser	Thr	Ala 420
Thr	Asn	Ser	Asp	Ser 425	Ser	Thr	Thr	Ser	Ser 430	Glu	Ala	Ser	Thr	Ala 435
Thr	Asn	Ser	Glu	Ser 440	Ser	Thr	Val	Ser	Ser 445	Gly	Ile	Ser	Thr	Val 450
Thr	Asn	Ser	Glu	Ser 455	Ser	Thr	Thr	Ser	Ser 460	Gly	Ala	Asn	Thr	Ala 465
Thr	Asn	Ser	Gly	Ser 470	Ser	Val	Thr	Ser	Ala 475	Gly	Ser	Gly	Thr	Ala 480
Ala	Leu	Thr	Gly	Met 485	His	Thr	Thr	Ser	His 490	Ser	Ala	Ser	Thr	Ala 495
Val	Ser	Glu	Ala	Lys 500	Pro	Gly	Gly	Ser	Leu 505	Val	Pro	Trp	Glu	Ile 510
Phe	Leu	Ile	Thr	Leu 515	Val	Ser	Val	Val	Ala 520	Ala	Val	Gly	Leu	Phe 525
Ala	Gly	Leu	Phe	Phe 530	Cys	Val	Arg	Asn	Ser 535	Leu	Ser	Leu	Arg	Asn 540
Thr	Phe	Asn	Thr	Ala 545	Val	Tyr	His	Pro	His 550	Gly	Leu	Asn	His	Gly 555
Leu	Gly	Pro	Gly	Pro 560	Gly	Gly	Asn	His	Gly 565	Ala	Pro	His	Arg	Pro 570
Arg	Trp	Ser	Pro	Asn 575	Trp	Phe	Trp	Arg	Arg 580	Pro	Val	Ser	Ser	Ile 585
Ala	Met	Glu	Met	Ser 590	Gly	Arg	Asn	Ser	Gly 595	Pro				

<210> 244

<211> 26

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgaacct tcccaqcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgcctactggg ggcctgtct ggatgggagg ccagcgatga 150

cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggaacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
			200					205						210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
			215					220						225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
			230					235						240
Ser	Val	Ala	Asn	Ile	Met	Pro								
			245											

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatc ttgaaggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccgggccc gcctggcaag ggggacgagt 50
cagtggacac tccaggaaga gcggccccgc ggggggcat gaccgtgcgc 100
tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcgacc gcggggcgga gctgccgcc gtgagtccgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgtcc tgcctccga atgctgcga 250
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300
cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgcctgcagc 350
gccgcctccg acctggggcg tcagcccccg gatcagcctg cctctgggct 400
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acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500
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tcagcccat gtgtacctac atcaacatgg agaactcac cctggcaagg 750
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aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350
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gaccacccg gtgcccacac ccggcctgg agcgtgcac accaacagtg 1450

90

Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys
365 370 375

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys	
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val	
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe	
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln	
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val Leu	
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr	
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro	
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile	
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg	
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp	Ser Val Val	
830	835	

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccgtagc gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100
agggcgggac gggagcccg actcgtctgc cgccgccgtc gtcgccgtcg 150

aaggatgatca gtgtttgcct ttgaacacat cttcttgctg aacattatgt 3100
agcagacctg cttaactttg acttgaaatg tacctgatga acaaaacttt 3150
tttaaaaaaa tgttttcttt tgagaccctt tgctccagtc ctatggcaga 3200
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ccagtgaaca atatttttct attgtacttt tcgaaccatt ttgtctcatt 4500

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50
tgacaccttc ctttccggcc ttgaggttcc cagcctggtg gcccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatatata 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

Pro Lys His Val Tyr	50	Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys	55	60
	65		70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu	80		85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95		100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110		115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125		130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140		145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155		160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170		175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185		190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200		205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215		220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230		235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245		250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260		265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275		280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290		295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305		310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320		325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335		340	345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcactg 200
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tgctccctct ttctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact 350
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gatgtggaga tctccattat agtccaggaa aatgctggga gcatattgtg 750
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agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

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Leu	Val	Gly	Glu	Asp 35	Ala	Val	Phe	Ser	Cys 40	Ser	Leu	Phe	Pro	Glu 45	
Thr	Ser	Ala	Glu	Ala 50	Met	Glu	Val	Arg	Phe 55	Phe	Arg	Asn	Gln	Phe 60	
His	Ala	Val	Val	His 65	Leu	Tyr	Arg	Asp	Gly 70	Glu	Asp	Trp	Glu	Ser 75	
Lys	Gln	Met	Pro	Gln 80	Tyr	Arg	Gly	Arg	Thr 85	Glu	Phe	Val	Lys	Asp 90	
Ser	Ile	Ala	Gly	Gly 95	Arg	Val	Ser	Leu	Arg 100	Leu	Lys	Asn	Ile	Thr 105	
Pro	Ser	Asp	Ile	Gly 110	Leu	Tyr	Gly	Cys	Trp 115	Phe	Ser	Ser	Gln	Ile 120	
Tyr	Asp	Glu	Glu	Ala 125	Thr	Trp	Glu	Leu	Arg 130	Val	Ala	Ala	Leu	Gly 135	
Ser	Leu	Pro	Leu	Ile 140	Ser	Ile	Val	Gly	Tyr 145	Val	Asp	Gly	Gly	Ile 150	
Gln	Leu	Leu	Cys	Leu 155	Ser	Ser	Gly	Trp	Phe 160	Pro	Gln	Pro	Thr	Ala 165	
Lys	Trp	Lys	Gly	Pro 170	Gln	Gly	Gln	Asp	Leu 175	Ser	Ser	Asp	Ser	Arg 180	
Ala	Asn	Ala	Asp	Gly 185	Tyr	Ser	Leu	Tyr	Asp 190	Val	Glu	Ile	Ser	Ile 195	
Ile	Val	Gln	Glu	Asn 200	Ala	Gly	Ser	Ile	Leu 205	Cys	Ser	Ile	His	Leu 210	
Ala	Glu	Gln	Ser	His 215	Glu	Val	Glu	Ser	Lys 220	Val	Leu	Ile	Gly	Glu 225	
Thr	Phe	Phe	Gln	Pro 230	Ser	Pro	Trp	Arg	Leu 235	Ala	Ser	Ile	Leu	Leu 240	
Gly	Leu	Leu	Cys	Gly 245	Ala	Leu	Cys	Gly	Val 250	Val	Met	Gly	Met	Ile 255	
Ile	Val	Phe	Phe	Lys 260	Ser	Lys	Gly	Lys	Ile 265	Gln	Ala	Glu	Leu	Asp 270	
Trp	Arg	Arg	Lys	His 275	Gly	Gln	Ala	Glu	Leu 280	Arg	Asp	Ala	Arg	Lys 285	
His	Ala	Val	Glu	Val 290	Thr	Leu	Asp	Pro	Glu 295	Thr	Ala	His	Pro	Lys 300	
Leu	Cys	Val	Ser	Asp 305	Leu	Lys	Thr	Val	Thr 310	His	Arg	Lys	Ala	Pro 315	

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320					325					330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val
				335					340					345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp
				350					355					360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn
				365					370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr
				380					385					390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr
				395					400					405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe
				410					415					420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
				425					430					435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr
				440					445					450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp
				455					460					465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
 ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg 50
 tgggtgagggc taggaaaaga gtttggttggg aaccctgggt tatcggcctc 100
 gtcattcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaaa tctccattaa ggaagaatt tgtcaagtct cagggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
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 cccaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgttt 150
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250
 acgccctcaa totgtctttt tggttaatgt ccatcagtgt gttggcagtt 300
 tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
 aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac 400
 cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcat ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg 600
aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650
tgcttggaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700
tactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950
gtattatgat agaagggagc ctgggacaga ccaaagatg tccttgaaga 1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050
agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150
caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450
atggtgggac tggagccata gtaaagggtg atttacttct accaactagt 1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat 1600
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc 1700
tgatcaggga ttttttgtat ataagtctgt gttaaatctg tataattcag 1750
tcgatttcag ttctgataat gttaagaata accattatga aaaggaaaat 1800
ttgtcctgta tagcatcatt attttagcc tttcctgtta ataaagcttt 1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650
gctgtggaga ttggcccaga ccaggatctg gatgttggtg aaatcacaga 700
aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750
gctccctggt ctccctgcac tgtcttgctt gtgggaagag cctgaagacc 800
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acccccactg ggtcctcacg gcagccact gcttcaggaa acataccgat 950
gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc 1000
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050
ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100
tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150
tcagccacc cactctgga tcattggatg gggctttacg aagcagaatg 1200
gaggggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg 1350
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atcgtagct ggggctatgg ctgcgggggc ccgagcacc caggagtata 1450
caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500
agctgtaatg ctgctgcccc tttgcagtgc tgggagccgc ttccttctg 1550
ccctgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1600
ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650
ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa 1700
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agacacagcc cactgaacaa ggtctcagg gtattgctaa gccagaagg 1800
aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
tcttcacca tccccagcc tactagagca agaaaccagt tgtaataata 1950
aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000
gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp
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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
				20					25					30

Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
				35					40					45

Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
				50					55					60

Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
				65					70					75

Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
				80					85					90

His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
				95					100					105

Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
				110					115					120

Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
				125					130					135

Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
				140					145					150

Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
				155					160					165

Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
				170					175					180

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
				185					190					195

Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
				200					205					210

Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
				215					220					225

Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
				230					235					240

Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255

265

10006001-10006001

Met 1	Ala	Leu	Pro	Ala 5	Leu	Gly	Leu	Asp	Pro 10	Trp	Ser	Leu	Leu	Gly 15
Leu	Phe	Leu	Phe	Gln 20	Leu	Leu	Gln	Leu	Leu 25	Leu	Pro	Thr	Thr	Thr 30
Ala	Gly	Gly	Gly	Gly 35	Gln	Gly	Pro	Met	Pro 40	Arg	Val	Arg	Tyr	Tyr 45
Ala	Gly	Asp	Glu	Arg 50	Arg	Ala	Leu	Ser	Phe 55	Phe	His	Gln	Lys	Gly 60
Leu	Gln	Asp	Phe	Asp 65	Thr	Leu	Leu	Leu	Ser 70	Gly	Asp	Gly	Asn	Thr 75
Leu	Tyr	Val	Gly	Ala 80	Arg	Glu	Ala	Ile	Leu 85	Ala	Leu	Asp	Ile	Gln 90
Asp	Pro	Gly	Val	Pro 95	Arg	Leu	Lys	Asn	Met 100	Ile	Pro	Trp	Pro	Ala 105
Ser	Asp	Arg	Lys	Lys 110	Ser	Glu	Cys	Ala	Phe 115	Lys	Lys	Lys	Ser	Asn 120
Glu	Thr	Gln	Cys	Phe 125	Asn	Phe	Ile	Arg	Val 130	Leu	Val	Ser	Tyr	Asn 135
Val	Thr	His	Leu	Tyr 140	Thr	Cys	Gly	Thr	Phe 145	Ala	Phe	Ser	Pro	Ala 150
Cys	Thr	Phe	Ile	Glu 155	Leu	Gln	Asp	Ser	Tyr 160	Leu	Leu	Pro	Ile	Ser 165
Glu	Asp	Lys	Val	Met 170	Glu	Gly	Lys	Gly	Gln 175	Ser	Pro	Phe	Asp	Pro 180
Ala	His	Lys	His	Thr 185	Ala	Val	Leu	Val	Asp 190	Gly	Met	Leu	Tyr	Ser 195
Gly	Thr	Met	Asn	Asn 200	Phe	Leu	Gly	Ser	Glu 205	Pro	Ile	Leu	Met	Arg 210
Thr	Leu	Gly	Ser	Gln 215	Pro	Val	Leu	Lys	Thr 220	Asp	Asn	Phe	Leu	Arg 225
Trp	Leu	His	His	Asp 230	Ala	Ser	Phe	Val	Ala 235	Ala	Ile	Pro	Ser	Thr 240
Gln	Val	Val	Tyr	Phe 245	Phe	Phe	Glu	Glu	Thr 250	Ala	Ser	Glu	Phe	Asp 255
Phe	Phe	Glu	Arg	Leu 260	His	Thr	Ser	Arg	Val 265	Ala	Arg	Val	Cys	Lys 270
Asn	Asp	Val	Gly	Gly 275	Glu	Lys	Leu	Leu	Gln 280	Lys	Lys	Trp	Thr	Thr 285
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
aggggtccctt agccggggcgc aggggcgcgca gccaggctg agatccgcgg 50
cttcogtaga agtgagcatg gctgggcagc gagtgttct tctagtgggc 100
ttcctttctcc ctgggggtcct gctctcagag gctgccaaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gttttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaattgagaa cttcgacatg gtgatagttg 500
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aatccccttg tcttatgttc cagtattccg ttcttgctg actgatcaca 650
tggaacttctg gggcogagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggg cagttttgtc tcatcttcta ctgaaagcag 800
agttgtggtt cattaactot gactttgcct ttgattttgc tcgacctctg 850
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgcctttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggctggt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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ggttgagggg ctgcctcttg catatgcaca cactcacaca ttctgtcaca 100
cccgtcacac acacatacca tgtttctccat cccccagggt ccagccctca 150
gtgctgtccc atccagcagg gctaccctga agctctgggt gcagccctcc 200
cgtccagtgg gcaggggggt tcatccctcc tttctctccc aaagcccaac 250
tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
gttcagcgag cctagagagg gcagactatc aggggtgccg cggtgagaat 400
ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgctact gccottggac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50
 tagccgccca gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttccccgctgg ggcgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggctcctg cgcgggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctcaaggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
 tcacctggct caataggtcc aagggtgaaa agcagctaca ggtcatctca 400
 gtgctccagt gggctcctgtc cttccttgta ctgggagtgg cctgcagtgc 450
 catcctcatg tacatattct gcactgattg ctggctcatc gctgtgctct 500
 acttcacttg gctgggtgttt gactggaaca cacccaagaa aggtggcagg 550
 aggtcacagt ggggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650
 atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700
 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750
 gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800
 agtacctgat gtctggaggt atctgccttg tcagccggga caccatagac 850
 tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtggctcg 900
 ggggtgctggct gactctctga gctccatgcc tggcaagaat gcagtcaccc 950
 tgcggaaccg caagggtctt gtgaaactgg ccctgcgtca tggagctgac 1000
 ctggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050
 cttcgaggag ggctcctggg gccgatgggt ccagaagaag ttccagaaat 1100
 acattggttt cgccccatgc atcttccatg gtcgaggcct cttctctctc 1150
 gacacctggg ggctgggtgcc ctactccaag cccatcacca ctgttgtggg 1200
 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
 acctgtacca caccatgtac atggaggccc tgggtgaagct cttcgacaag 1300
 cacaagacca agttcggcct ccgggagact gaggtcctgg aggtgaactg 1350
 agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400
 tttgctctgt aaatttgaa gtgtcatggg tgtctgtggg ttatttaaaa 1450
 gaaattataa caattttgct aaacaaaaa aaaaaaaaa aaaaaaaaa 1500
 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1550
 aaaaaaaaa aaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1				5					10					15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val	Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile	Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile	Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His	Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu	Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu	Pro Glu Thr Glu Val Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcgagg atggggggcgg ggggcggcggg gcgcgcgact cgctgaggcc 50
ccgacgcagg gccggggcggg gcccgaggcc gaggagcgcg gcggccagag 100
cgggggcgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggcctg 250
caccgcctcc tgagcagcg catgggcctg ctggccttcc tgaagacca 300
gttcgtgctg cactgctgg tcggctttgt cttcgtggtg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggctcatg ctgctggagt ggtggtcctg cacggagtgt acactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gctccaaggc cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcgcc tggacgtggc actttctgga gattgtgttc 700
tgcaagcgga agtgggagga ggaccgggac accgtggctg aagggtgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800
ggacgcgctt cacggagacc aagcacccgc ttagcatgga ggtggcggt 850
gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
atgtaaccct gaacttcaga ggaaacaaga acccgctcct gctggggatc 1000
ctctacggga agaagtacga ggcggacatg tgcgtgagga gatttcctct 1050
ggaagacatc ccgctggtg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

ttgttctgtt gccaggctg gactacagt gcacagtctt ggtcactgc 2650
 agcctcgacc tctgggctg cagtgatcct cccacctcag cctcccttgt 2700
 agctgtatatt ttttgtatatt tgtatattgt agctgtagtt tttgtatatt 2750
 ttgtggagac agcatttcac catgatgcc aggtgtgtct tgaactcctg 2800
 agctcaagtg atctgcctgc ttcagcctcc caaagtgtg ggattacaga 2850
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gccccaacta 2950
 ccaggagagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000
 cagtgaagtcg aggttgtgctg actgcattcc agcctggaca acagagtgtg 3050
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
1				5					10					15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20					25					30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35					40					45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50					55					60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65					70					75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala
				80					85					90
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly
				95					100					105
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val
				110					115					120
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr
				125					130					135
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu
				140					145					150
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr
				155					160					165

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt ggggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg ccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gcccagggtg ggcatctcta acaaactccc acgtgatgct gatgctgggc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcacttttg gaggctgagg caggctgac 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5				10						15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20				25						30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35				40						45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50				55						60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65				70						75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80				85						90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95				100						105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110				115						120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125				130						135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
 aagggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500
 ggogatggct cccactgccc aggcacagc cttgctgtag tcaatcactg 550
 ccctggggcc aggacgggc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800
 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggtg ccgatggcg atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100
 ctccctcct tccctctgag aggcctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgg tcagtgttgg ccaggaggt 1200
 cagcaaggcc tgagagctga tcagaaggc ctgctgtgcg aacacggaaa 1250

tcaagtcgcg	ggctcctcggc	ccaaagatcg	aggcggtgca	gaaagtgaac	1750
aaggctggga	tggagaagga	gaaggccgag	gagaagctgg	ccggggagga	1800
gctggccggg	gaggaggccc	cccaggagaa	ggcggaggac	aagcccagca	1850
ccgatctctc	agccccagtg	aatggcgagg	ccacatcaca	gaagggggag	1900
agcgcagagg	acaaggagca	cgaggagggt	cgggactcgg	aggagggggc	1950
aaggtgtggc	tcctctgaag	acctgcacga	cagcgtacgg	gaggggtccc	2000
acctggacag	gcctgggagc	gaccggcagg	agcgcgagag	ggcacggggg	2050
gactcggagg	ccctggacga	ggagagctga	gccgcgggca	gccaggccca	2100
gccccgccc	gagctcaggc	tgcccctctc	cttccccggc	tcgcaggaga	2150
gcagagcaga	gaactgtggg	gaacgctgtg	ctgtttgtat	ttgttccctt	2200
gggttttttt	ttcctgccta	atctctgtga	ttccaacca	acatgaaatg	2250
actataaacg	gttttttaat	ga	2272		

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met Pro His Ala Phe Lys Pro Gly Asp Leu Val Phe Ala Lys Met
1 5 10 15

Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp
20 25 30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
35 40 45

Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60

Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75

Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90

Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105

Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120

Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135

Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met Ser	
155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln Ala	
170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser Glu	
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys Ala	
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys Lys	
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp Ser	
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala	Met Ala Arg Ser Ala Ser	
245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser Val	
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu Pro	
275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser Ser	
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser Glu	
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala Arg	
320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln	
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly	
350	355	360
Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	
				440					445					450	
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	
				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
				470					475					480	
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
				500					505					510	
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
				530					535					540	
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
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Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					
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<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
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Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
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Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
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Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
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Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
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Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
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His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
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Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
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Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
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Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	515	520	525
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	530	535	540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	545	550	555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	560	565	570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

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Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu	
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Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu	
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp	
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His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp	
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 <213> Artificial

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 <223> Synthetic construct.

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<210> 312
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 312
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<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

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<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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5

10

15

305

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Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	
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Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	
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Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	
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Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	
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Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	
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Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
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Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
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Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
				230					235					240	
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Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	
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Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	

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Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His Ile				
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Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys Asn				
185	190				195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg Ala				
200	205				210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val Val				
215	220				225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys Arg				
230	235				240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys His				
245	250				255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val				
260	265				270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala				
275	280				285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn				
290	295				300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu				
305	310				315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu				
320	325				330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys				
335	340				345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala				
350	355				360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys				
365	370				375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val				
380	385				390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser				
395	400				405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr				
410	415				420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro				
425	430				435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
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Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp 740		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr 755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro 770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg 785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro 800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu 815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys 830	835	

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggcgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtctgtttt 200
gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcaactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atctttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
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atactgaaaa tggaatagaa ttgatccca tgctggatga gagagggtat 850
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atataataaa tgcatgctat tcaatgaatt tctgcctatg aggcactctg 1100
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tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggcgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
tggcgtgcc ccaagacctc caggetgccc gcgccctcat ggtcatctcc 350
tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
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tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550
cgcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
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tgcaaacacc gcacctgctt accagccacc agctgcctac aaagacaatc 750
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gtccccggcg ggactgtcaa tggaggcagg ggttcagca caaagtttac 900
ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950
ctttagagca cagggacaga gggggaaata agaggaggag aaagctctct 1000

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgctca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
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 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350
 gtcttggttg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600
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 gggggtgtga tgatgtgcat cgcctgccgg ggcctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
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 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
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80									85					90	
Ala	Ile	Gly	Leu	Leu 95	Val	Ser	Ile	Phe	Ala 100	Leu	Lys	Cys	Ile	Arg 105	
Ile	Gly	Ser	Met	Glu 110	Asp	Ser	Ala	Lys	Ala 115	Asn	Met	Thr	Leu	Thr 120	
Ser	Gly	Ile	Met	Phe 125	Ile	Val	Ser	Gly	Leu 130	Cys	Ala	Ile	Ala	Gly 135	
Val	Ser	Val	Phe	Ala 140	Asn	Met	Leu	Val	Thr 145	Asn	Phe	Trp	Met	Ser 150	
Thr	Ala	Asn	Met	Tyr 155	Thr	Gly	Met	Gly	Gly 160	Met	Val	Gln	Thr	Val 165	
Gln	Thr	Arg	Tyr	Thr 170	Phe	Gly	Ala	Ala	Leu 175	Phe	Val	Gly	Trp	Val 180	
Ala	Gly	Gly	Leu	Thr 185	Leu	Ile	Gly	Gly	Val 190	Met	Met	Cys	Ile	Ala 195	
Cys	Arg	Gly	Leu	Ala 200	Pro	Glu	Glu	Thr	Asn 205	Tyr	Lys	Ala	Val	Ser 210	
Tyr	His	Ala	Ser	Gly 215	His	Ser	Val	Ala	Tyr 220	Lys	Pro	Gly	Gly	Phe 225	
Lys	Ala	Ser	Thr	Gly 230	Phe	Gly	Ser	Asn	Thr 235	Lys	Asn	Lys	Lys	Ile 240	
Tyr	Asp	Gly	Gly	Ala 245	Arg	Thr	Glu	Asp	Glu 250	Val	Gln	Ser	Tyr	Pro 255	
Ser	Lys	His	Asp	Tyr 260	Val										

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<210> 327
<211> 2010
<212> DNA
<213> Homo sapiens
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caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
gtgggcacag tggtgtcac tgtcatgcct cagtggagag tgtcggcctt 200
cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
tgaattgcgt gaggcaggct aacatcagga tgcaatgcaa aatctatgat 300
tcctgtgtgg ctctttctoc ggacctacag gcagccagag gactgatgtg 350
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tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca 400
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 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagtttgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaatttt aattacagga 900
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 tgctaaagac tgcattattt tactactgta atttctocac gacatagcat 1100
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 tgtottggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

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 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
 gcctgtggat gtctgctgtg gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctgggtctacc 300
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 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
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 cagctatgta gaaccccgcc cccacctcca aactgcacc cttctgcct 1250

1005053-1250T

gccccctcg tctcaccccc tttaactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
			20						25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtggg 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
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gcaagttcta tagctccttg ttggctctcc cgcctgccct ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgcctc tccttgatcg ccctgcttat 400
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ccaagtatgg actatggtca atgttttta taaagtcctg ctagaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtttc aatttggtac tgggtgtagg aatgaaaatg acttacttgg 950
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cgctgctcca attttcatat tctaaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

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Tyr Ser Ser Leu	Leu Ala Leu Pro Pro Ala	Leu Glu Thr Ala Arg	
	20	25	30
Ala Leu Met Cys	Val Ala Val Ala Leu Ser	Leu Ile Ala Leu Leu	
	35	40	45
Ile Gly Ile Cys	Gly Met Lys Gln Val Gln	Cys Thr Gly Ser Asn	
	50	55	60
Glu Arg Ala Lys	Ala Tyr Leu Leu Gly Thr	Ser Gly Val Leu Phe	
	65	70	75
Ile Leu Thr Gly	Ile Phe Val Leu Ile Pro	Val Ser Trp Thr Ala	
	80	85	90
Asn Ile Ile Ile	Arg Asp Phe Tyr Asn Pro	Ala Ile His Ile Gly	
	95	100	105
Gln Lys Arg Glu	Leu Gly Ala Ala Leu Phe	Leu Gly Trp Ala Ser	
	110	115	120
Ala Ala Val Leu	Phe Ile Gly Gly Gly Leu	Leu Cys Gly Phe Cys	
	125	130	135
Cys Cys Asn Arg	Lys Lys Gln Gly Tyr Arg	Tyr Pro Val Pro Gly	
	140	145	150
Tyr Arg Val Pro	His Thr Asp Lys Arg Arg	Asn Thr Thr Met Leu	
	155	160	165
Ser Lys Thr Ser	Thr Ser Tyr Val		
	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

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 ctcagaagct gctagtctgt ctcaaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaatttcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatacct tttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15
Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg ottgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgctc agggaccca acgcatccc agcccagcgc 250

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
 50 55 60
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
 65 70 75
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
 80 85 90
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
 95 100 105
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
 110 115 120
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
 125 130 135
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
 140 145 150
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
 155 160 165
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
 170 175 180
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
 185 190 195
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
 200 205 210
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
 215 220 225
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
 230 235 240
 Phe Ala Met Tyr Arg Pro
 245

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
 gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50
 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
 caagacccta agaaccatca gccctcagct gcacctctc cctccaagg 150
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
 tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaagg tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaaagct aacttgaaca tgacctgttg catttgga 450
gttctagcaa catgctocta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tctgctgct cctgatgctg ggatgcgctc tgatgatgg 550
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aagccagcaa gcacagccct gaagccagggt accgcctgga ctttggggaa 650
tcccaggatt gggactgga agctgaggat gagggtgaag agtacagccc 700
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750
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ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
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aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950
agtgcccgca tccccctcca gagggctctg cccgagggtgc ggcaccact 1000
gtgtctgcag cagcacctc aggacagcct gccacagcc agcgtcatcc 1050
tctgtttcca tgatgaggcc tgggtccactc tctgctggac tgtacacagc 1100

tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val	560		565		570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln	575		580		585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser	590		595		600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu	605		610		615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe	620		625		630
Asp Gln Ile Asn Ala Val Asp Glu Arg	635				

<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgtcg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tcctctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200
caggggaggc ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag cogatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300
cctggcactg cacccccagc caccocatca ggctttgagg aggggccgcc 350
ctcatcccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400
aggatggagg ggacccaac tctgccaatc ccggatttct ggactatggt 450
tttgagccc ctcatgggct cgcaacccca caccccaact cagactccat 500
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
ggccattcct gttcgggggc cgtggggaag gtgtggacc ccagctctat 600
gtcacaatta ccatctccat catcattgtt ctctgggcca ctggcatcat 650
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
agcaagggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
tccccggctg gagtcaactgt gctggggggc ttcggggact cacctacccc 800
caccctgac catgaggagc ccgagggggg acccggcct gggatgcccc 850
acccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950
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gcccctggcc ctccaaggg ggctggacca gtcctctctt gggaggcacc 1050
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tctcaggatt cccctggtga atctgtgatg cccccaatgt tggggtgcag 1300

tccgggggttc tggccccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggcgggtcgc tggggcccg cgctatcgc gccatcgtga 350
 tcgccgcct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
1				5					10					15
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20					25					30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110					115					120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

ggccgttggt tgggtgcgcg ctgaaggggtg tggcgcgagc agcgtcgttg 50
 gttggccggc ggcgggcccgc gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactg cacagcaact 150
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtccctg 200
tggggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
taccagggga agatgtactt ccccggttat ttccccaacg agctgcgaaa 400
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500
agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550
agtagccccc agaggcgctg ggagtgttgc caccgccctc ccctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tgcatcttc cagtacgaga ccatctcctg caacaactgc acagactgcg 750
acgtcgcttg ctttggctat aactgcgagt agggctcagg catcacacc 800
acctgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
gggctccccg ccttcacct ggctgtcatc gggtagggcg gggcctggg 900
ttcaggggcg caccacttcc aagcctgtgt cccacaggtc ctggcgag 950
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcaca 1000
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100
ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150
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aggtctgtgg tcagagcctg ggagggttcc ctacgatgg taggggtgcc 1300
ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400
agaggagggg ggctagggg tcctctagat cagtggggg actgcagggtg 1450
gggctctccc tatacctgg acacctgtg gatgtcacct ctgcaaccac 1500
acctatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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cctcttatttt ctctctacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggogtgtcat ttgggatcag cactgattct 300
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctctctga taatgaacaa ggctctccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctcttttattc tgggtggacag tggatatgaa gaaaatggga aggtgatatc 650
atTTTTcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tggtgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtotaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc ttttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagccaa 100
cctcagcggg gaccgggct cagggacgcg gcggcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcggcg gcgcttgggc 250
tcttgacagc tggagtatca gccttgaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggccgggttga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
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tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tcggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

Trp	Ser	Pro	Gln	Thr 95	Pro	Ala	Pro	Pro	Cys 100	Ser	Arg	Cys	Phe	Ala 105
Arg	Ala	Ile	Glu	Ser 110	Ser	Arg	Asp	Leu	Leu 115	His	Arg	Ile	Lys	Asp 120
Glu	Val	Gly	Ala	Pro 125	Gly	Ile	Val	Val	Gly 130	Val	Ser	Val	Asp	Gly 135
Lys	Glu	Val	Trp	Ser 140	Glu	Gly	Leu	Gly	Tyr 145	Ala	Asp	Val	Glu	Asn 150
Arg	Val	Pro	Cys	Lys 155	Pro	Glu	Thr	Val	Met 160	Arg	Ile	Ala	Ser	Ile 165
Ser	Lys	Ser	Leu	Thr 170	Met	Val	Ala	Leu	Ala 175	Lys	Leu	Trp	Glu	Ala 180
Gly	Lys	Leu	Asp	Leu 185	Asp	Ile	Pro	Val	Gln 190	His	Tyr	Val	Pro	Glu 195
Phe	Pro	Glu	Lys	Glu 200	Tyr	Glu	Gly	Glu	Lys 205	Val	Ser	Val	Thr	Thr 210
Arg	Leu	Leu	Ile	Ser 215	His	Leu	Ser	Gly	Ile 220	Arg	His	Tyr	Glu	Lys 225
Asp	Ile	Lys	Lys	Val 230	Lys	Glu	Glu	Lys	Ala 235	Tyr	Lys	Ala	Leu	Lys 240
Met	Met	Lys	Glu	Asn 245	Val	Ala	Phe	Glu	Gln 250	Glu	Lys	Glu	Gly	Lys 255
Ser	Asn	Glu	Lys	Asn 260	Asp	Phe	Thr	Lys	Phe 265	Lys	Thr	Glu	Gln	Glu 270
Asn	Glu	Ala	Lys	Cys 275	Arg	Asn	Ser	Lys	Pro 280	Gly	Lys	Lys	Lys	Asn 285
Asp	Phe	Glu	Gln	Gly 290	Glu	Leu	Tyr	Leu	Arg 295	Glu	Lys	Phe	Glu	Asn 300
Ser	Ile	Glu	Ser	Leu 305	Arg	Leu	Phe	Lys	Asn 310	Asp	Pro	Leu	Phe	Phe 315
Lys	Pro	Gly	Ser	Gln 320	Phe	Leu	Tyr	Ser	Thr 325	Phe	Gly	Tyr	Thr	Leu 330
Leu	Ala	Ala	Ile	Val 335	Glu	Arg	Ala	Ser	Gly 340	Cys	Lys	Tyr	Leu	Asp 345
Tyr	Met	Gln	Lys	Ile 350	Phe	His	Asp	Leu	Asp 355	Met	Leu	Thr	Thr	Val 360
Gln	Glu	Glu	Asn	Glu 365	Pro	Val	Ile	Tyr	Asn 370	Arg	Ala	Arg		

351

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagaa gtctggcag aaggttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccgggccc gggactgggt gcgagggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctgggt gctatgtctc ctcccttctc cctgcgtgct ccctggtgga 500
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tgggtgggctg gtcgggtggt acgcaccccg ggggctgccg gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgccctg 700
agatggaaca ggcccagaag gccagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
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ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
1 5 10 15

Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggaaccgga gccggagccg gagccacagc ggggaggggtg 50
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 cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
 ctggacttct atcaggteta cttcctggcc ctggcagctg attggcttca 300
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
 ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
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 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
 ctgctcttct cagccttcga ggcttggtat atccatgagc acgtggaacg 600
 gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
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 gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
 tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
 atgacoggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
 ctctgtcgg accgccgctg gctgctgctg ggcaccatac aagctctatt 900
 tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
 ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
 tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
 tcttcatgtt gactttctct accagcccag gccaggagag tccgggtggag 1150
 tccttcatag cttttctact tattgagttg gcttgtggat tatactttcc 1200
 cagcatgagc ttctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
 gtgtactcaa ctggttcggg gtacctctgc actcactggc ttgcctaggg 1300
 ctctttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
 cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
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 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

ccttggtccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
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 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
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 aatttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
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 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
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Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20						25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35						40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
			50						55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
			65						70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
			80						85					90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
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 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccacagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50

ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcctggggg gcccacctg ggaggggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctcog gggtatggtc atgtacacca gcaaggaccg ctatttctat 450

tttggaagc ttgatggcca gatctcctct gcctacccca gccaagaggg 500

gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650

ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

atctcagaaa	ttacaggaga	taccctcaag	tatatctgct	ggttgcttag	700
gtttgtccct	tcgctataac	agccttcaaa	aacttaagta	taatcaattt	750
aaagggctca	accagctcac	ctggctatac	cttgaccata	accatatcag	800
caatattgac	gaaaatgctt	ttaatggaat	acgcagactc	aaagagctga	850
ttcttagttc	caatagaatc	tcctattttc	ttaacaatac	cttcagacct	900
gtgacaaatt	tacggaactt	ggatctgtcc	tataatcagc	tgcattctct	950
gggatctgaa	cagtttcggg	gcttgcgga	gctgctgagt	ttacatttac	1000
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aacctggaac	ttttggacct	gggatataac	cggatccgaa	gtttagccag	1100
gaatgtcttt	gctggcatga	tcagactcaa	agaacttcac	ctggagcaca	1150
atcaattttc	caagctcaac	ctggcccttt	ttccaagggt	ggtcagcctt	1200
cagaaccttt	acttgcagtg	gaataaaatc	agtgtcatag	gacagaccat	1250
gtcctggacc	tgagctcct	tacaaaggct	tgatttatca	ggcaatgaga	1300
tcgaagcttt	cagtggaccc	agtgttttcc	agtgtgtccc	gaatctgcag	1350
cgcctcaacc	tggattccaa	caagctcaca	tttattggtc	aagagatttt	1400
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aatgcagcag	aaatatttgc	tcctttgtaa	actggctgaa	aagttttaaa	1500
ggtctaaggg	agaataacaat	tatctgtgcc	agtcccaaag	agctgcaagg	1550
agtaaattgt	atcgatgcag	tgaagaacta	cagcatctgt	ggcaaaaagta	1600
ctacagagag	gtttgatctg	gccagggctc	tcccaaagcc	gacgtttaag	1650
cccaagctcc	ccaggccgaa	gcatgagagc	aaacccccct	tgcccccgac	1700
ggtgggagcc	acagagcccg	gccagagac	cgatgctgac	gccgagcaca	1750
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ctcgtcatcc	tgctggttat	ctacgtgtca	tggaagcggg	accctgcgag	1850
catgaagcag	ctgcagcagc	gctccctcat	gcgaaggcac	aggaaaaaga	1900
aaagacagtc	cctaaagcaa	atgactccca	gcaccagga	attttatgta	1950
gattataaac	ccaccaacac	ggagaccagc	gagatgctgc	tgaatgggac	2000
gggaccctgc	acctataaca	aatcgggctc	cagggagtgt	gaggtatgaa	2050
ccattgtgat	aaaaagagct	cttaaaagct	gggaaataag	tggtgcttta	2100

ttgaactctg gtgactatca agggaacgag atgccccccc tccccttccc 2150
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 tcataatact ggtcattttc ctctcatata taatcaaccc attgaaattt 2250
 aaataaccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
 1 5 10 15
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

10006065-10604

200	205	210
His Leu Glu His Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe	
215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys	
230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu	
245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly	
260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu	
275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser	
290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu	
305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe	
320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu	
335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile	
350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu	
365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu	
380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly	
395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile	
410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu	
425	430	435
Leu Val Ile Tyr Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys	
440	445	450
Gln Leu Gln Gln Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys	
455	460	465
Arg Gln Ser Leu Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr	
470	475	480
Val Asp Tyr Lys Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu	
485	490	495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtcacctca 100
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtgcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacacggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctcogtg gcggcggcga cgtgacgag aagcccacgg ccagctcagt 200
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacotca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatgtgg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650
tggcaggata tgccgatctg aaaagaacaa ttgctgtcct tctggatgac 700
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800
cagtaaccac aaataaaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca ccttggtgctg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950
aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aatttttaag ttatttgttt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
 aaatgaaaac actgaaaaac atggattcat ttctataaca cattttattta 1200
 agtatataac acgttttttg gacaagtga gaagtgttaa tcattctgtc 1250
 atttgttctc aatagatgta actgttagac tacggctatt tgaaaaaatg 1300
 tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
 tataatgttg aaaataatgt tttgaaatca tgacccaaag aatgtattga 1400
 ttgacactat ccttcagaat aactgaaggt taattattgt atatttttaa 1450
 aaattacact tataagagta taatcttgaa atgggtagca gccactgtcc 1500
 attacctatc gtaaacattg gggcaattta ataacagcat taaaatagtt 1550
 gtaaactcta atcttatact tattgaagaa taaaagatat ttttatgatg 1600
 agagtaacaa taaagtattc atgatttttc acatacatga atgttcattt 1650
 aaaagtttaa tcctttgagt gtctatgcta tcaggaaagc acattatttc 1700
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 tttggagaat ggaactcttg aggactttag ccagggtgtat ataataaagg 1800
 tacttttgtg ctgcattaaa ttgcttgga agtggttaaca ttatattata 1850
 taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900
 attcatttta tataatggcc acttaaaata agaacattta aaatataaac 1950
 tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000
 accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050
 atttccottg tagcaaatct aattgccaca tgggtgccta tatttcatag 2100
 tattttattc ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150
 actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200
 catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
 tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
 acctttatgt gaagaaatta atttatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10					15	

1005050007

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
155 160 165

His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
170 175 180

Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
185 190 195

Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
200 205 210

Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
215 220 225

Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
230 235 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
260 265 270

Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
275 280 285

Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
290 295 300

His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
305 310 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
320 325 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
335 340 345

Ala Ala Arg Gly Pro Thr Ile Leu
350

<210> 398
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 398
ccctgccagc cgagagcttc acc 23

<210> 399
<211> 23
<212> DNA

[illegible]

<223> Synthetic construct.

ggttggtgcc cgaaagggtcc agc 23

<213> Artificial

<223> Synthetic construct.

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<213> Homo sapiens

gatggcgag ccacagcttc tgtgagattc gattttctccc cagttcccct 50

gtgggtctga ggggaccaga aggggtgagct acgttggctt tctggaaggg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac ggaagacttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaa cctctagtct tgccttcagg cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaataac gaaatggatt 500

tcttgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaaagcc tgcgaatcga 600

tgctgcctcc tgcgccatth gctaagactc tatctggaca gggatatttaa 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaatttcctt ttgtaccatc aagaaggacc tccggctctc tcatgccgac 750

10005063.120001

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
95 100 105

Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
110 115 120

Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
125 130 135

Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
140 145 150

Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
155 160 165

Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
170 175 180

Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
185 190 195

Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
200 205 210

Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
215 220 225

Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
230 235 240

Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
245 250 255

Trp Met Glu Glu Thr Glu
260

<210> 403
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 403
ctcctgtggt ctccagattt caggccta 28

<210> 404
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

1006063.120604

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcccat ttacagacac gtagtgatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtc ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatg gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggtgttct aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgacct cttggatcaat ggtgttcttg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttta 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcggtatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200

agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatfff ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400

ctgttttagga agaacagggtg ctcgagtttg gcttttcatt ggtttcatgt 450

tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500

gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttggga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
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 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
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 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgagct gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcaactgagc 1300
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccagaag gactagtgtg aaagcttctt 1450
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
 1 5 10 15
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
 35 40 45
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
 50 55 60
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
 65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 411
gtttgaggaa gctgggatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 412
ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 413
atggcaggct tcttagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414

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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
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tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgtgggtt ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgttttaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
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gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag ccagacaca aacaaatacg agggatggcc agagctgctg 950
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gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaacct 1150
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tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
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 <213> Homo sapiens

<400> 415

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Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

<210> 416
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
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<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
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cacgccagga gctcgtcgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtccct 250
gcaccccttc ctgggacact atgttggtt cgcacctct gctggagggtg 300
atttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctotta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgacctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactgggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
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atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
totgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

aacctgcttt gggactccct ccacaaaaac tggctccgga tcagggaaca 200
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 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
 ctgctgcagg aatgacacct ggtaccaga cccacccatt gaccctggga 350
 ggggtgaatg tacaacagca actgcacca catgtgttac caattttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatactg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaata 700
 agcaaataga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
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<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
			35						40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80					85					90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

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 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggctccgog gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgtc gagcgccctct gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttccgctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650


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<211> 19
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 435
cccacctgta ccacatgt 19

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 436
actccaggca ccacatgttc tccc 24

<210> 437
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 437
aagggtggc attcaagtc 19

<210> 438
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<220>
<223> Synthetic oligonucleotide probe

<400> 438
tgacctggca aaggaagaa 19

<210> 439
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<220>
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cagccaccct ccagtccaag g 21

<210> 440
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<220>
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gggtcgtgtt ttggagaga 19

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ctggccctca gagcaccaat 20

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tcctccatca cttcccctag ctcca 25

<210> 443
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<220>
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<400> 443
ctggcaggag tttaaagttcc aaga 24

<210> 444
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<400> 444
aaaggacacc gggatgtg 18

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<220>
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<400> 445
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<210> 446
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<220>
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<400> 446
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<210> 447
<211> 20
<212> DNA
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<220>
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<400> 447
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<210> 448
<211> 21
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<220>
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<210> 449
<211> 18
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<220>
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<400> 449
  ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
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<220>
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<400> 450
  ccctagctga ccccttca 18

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456
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<210> 457
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<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457
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<210> 458
<211> 18
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<223> Synthetic oligonucleotide probe

<400> 458
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<400> 459
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<210> 460
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<400> 460
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<210> 461
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tggacacgtg gcagtgga 18

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<400> 462
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 463
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<210> 464
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<220>
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<400> 465
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<210> 466
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<212> DNA
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<220>
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<400> 466

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 467

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<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
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<220>
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<400> 472
tcagggtcta catcagcctc ctgc 24

<210> 473
<211> 19
<212> DNA
<213> Artificial Sequence

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<400> 473
aaggccaagg tgagtccat 19

<210> 474
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<400> 474
cctactgagg agccctatgc 20

<210> 475
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<212> DNA
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<220>
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<400> 475
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<210> 476
<211> 24
<212> DNA
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<220>
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<400> 476
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<210> 477
<211> 50
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

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